

SEQUENCE LISTING

<110> KLAGSBRUN, Michael
SOKER, Shay
MIAO, Hua Quan
TAKASHIMA, Seiji

<120> NEUROPHILINS AND USE THEREOF IN METHODS
FOR DIAGNOSIS, PROGNOSIS AND TREATMENT OF CANCER

<130> 48802

<150> 60/069,155
<151> 1997-12-09

<150> 60/069,687
<151> 1997-12-29

<150> 60/078,541
<151> 1998-03-19

<160> 11

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 5653
<212> DNA
<213> human

<400> 1

aagggagagg aagccggagc taaatgacag gatgcaggcg acttgagaca	caaaaagaga	60
agcgttccctc tcggatccag gcattgcctc gctgtttct ttctccaag acgggctgag		120
gattgtacag ctcttaggcgg agttgggct cttcgatcg cttagattct cctttgtct		180
gcattttcccc ccacgtcctc gttctcccg gcgtcctgc ggaccggag aagggagaat		240
ggagaggggg ctggcgctcc tctgcgcgt gtcgcctc gtccctgccc cgccggcgc		300
ttttcgcaac gataaatgtg gcgataactat aaaaattgaa agcccccgggt accttacatc		360
tcctggttat cctcattctt atcacccaag tgaaaaatgc gaatggctga ttcaaggctcc		420
ggaccatac cagagaatta tcatcaactt caaccctcac ttcaaggcttgg aggacagaga		480
ctgcaagtat gactacgtgg aagtgttgc tggagaaaat gaaaatggac attttagggg		540
aaagtctgt ggaaagatag cccctccctc tggatgtct tcaggccat ttcttttat		600
caaatttgtc tctgactacg aaacacatgg tgcaggattt tccatacgtt atgaaatttt		660
caagagaggt cctgaatgtt cccagaacta cacaacacct agtggagtga taaaatcccc		720
cggattccct gaaaaatatac ccaacagcct tgaatgcact tatattgtct ttgcgccaaa		780
gatgtcagag attatcctgg aatttggaaag ctggacactg gagcctgact caaatccccc		840
agggggatg ttctgtcgct acgaccggct agaaatctgg gatggattcc ctgatgttgg		900
ccctcacatt gggcgtaact gtggacagaa aacaccaggt cgaatccgat cctcatcggt		960
cattctctcc atggttttt acaccgacag cgccgatagca aaagaaggt tctcagcaaa		1020
ctacagtgtc ttgcagagca gtgtctcaga agatttcaaa tggatggaaat ctctggcat		1080
ggaatcagga gaaattcatt ctgaccagat cacagttct tcccagtata gcaccaactg		1140
gtctgcagag cgctcccgcc tgaactaccc tgaaatggg tggactcccg gagaggattc		1200
ctaccgagag tggatcagg tagacttggg ctttctgcgc ttgtcacgg ctgtcgggac		1260
acagggcgcc atttcaaaag aaaccaagaa gaaatattat gtcaagactt acaagatcga		1320
cgttagtcc aacggggaaag actggatcac cataaaagaa gaaaacaaac ctgttcttt		1380
tcagggaaac accaacccta cagatgttgtt ggttgcagta ttccccaaac cactgataac		1440
tcgatgtc cgaatcaagc ctgcaactt gaaactggc atatctatga gatttgaagt		1500
atacgggtgc aagataacag attatcctt ctctggatg ttgggtatgg tggatggact		1560
tatttctgac tcccgatca catcatccaa ccaagggac agaaactggaa tgcctgaaaa		1620
catccgcctg gtaaccagtc gctctggctg ggcacttcca cccgcacccatc attcctacat		1680
aatgagtgg ctccaaatag acctggggga ggagaagatc gtgagggca tcatcattca		1740

gggtgggaag caccgagaga acaagggtt catgaggaag ttcaagatcg ggtacagcaa	1800
caacggctcg gactggaga tgcacatggc tgacagcaaa cgcaaggcga agtctttga	1860
gggcacaaca aactatgata cacctgact gcggacttt ccagctctt ccacgcatt	1920
catcaggatc taccggaga gagccactca tggccggactg gggctcgaaa tggagctgct	1980
gggctgtgaa gtggaaagccc ctacagctgg accgaccact cccaaacggga acttggtgaa	2040
tgaatgtat gacgaccagg ccaactgcca cagtgaaaca ggtatgact tccagctcac	2100
aggtggcacc actgtgtctgg ccacagaaaa gccacggtc atagacagaca ccatacaatc	2160
agagttcca acatatgtt ttaactgtga atttggctgg ggctctcaca agaccttctg	2220
ccactggaa catgacaatc acgtgcaggt caagtggagt gtgttgacc gcaagacggg	2280
acccattcag gatcacaatc gagatggca cttcatatat tcccaagctg acgaaaatca	2340
gaaggcaca gtggctcgcc tggtgagcc tggatggat tcccaagact ctgcccactg	2400
catgaccttc tggatcaca tggatggat ccacgtcgcc acactcaggg tcaaactgctg	2460
ctaccagaag ccagaggagt acgtcaggt ggtctggatg gccattggac accaagggtg	2520
ccactgaaag gaaggcgtg tttgtccca caagtctctg aaactttatc aggtgatattt	2580
cgagggcaca atcgaaaaag gaaaccttgg tggatggat gtggatgaca ttgtattaa	2640
caaccacatt tcacaagaag attgtcggaaa accagcagac ctggataaaa agaaccaga	2700
aattaaaaatt gatgaaacag ggagcacgca aggatacgaa ggtgaaggag aaggtgacaa	2760
gaacatctcc aggaagccag gcaatgtgtt gaagaccta gatccccatcc tcatcaccat	2820
catagccatg agtgccttgg gggctccctt gggggctgtc tggatggatgactg	2880
tgcctgttgg cataatggga tggatggat gaaacttgcactt gccctggaga actataactt	2940
tgaacttgcactt gatggatggat gttggatggat gttggatggat gttggatggat	3000
ggaggcatga aggacacac agatggaaaac acagtcaaaag gacggaaatgg gaaaggacggg	3060
agttagctgg ggagctgttgc atctttactt atacaggctg ggaagtgtgt tgatgaccac	3120
ttagccaggc ttttctcagg agtctcaatg agttagggccg acagacatgg acaaggagct	3180
gtgttcacca tcggactcat gtgcagtcag ctttttctt gttggatggat tttgataat	3240
cagatgttgg tggatggat gttggatggat gacataatca ttcatttcg cccctctgc	3300
ccctctcttctt ctctctcttcc tcccccttgg gatgtttttt tggaaactg gcaaatccca	3360
agatgttggc accaagcgtt tccctgttgg ccctttggat ggacatgcta cctgaaaccc	3420
agtgccttgcataatactaga atcaccgcattt ttcagtggac ttctgaaatgt tgacttgtgt	3480
ataatttgcgc gctgtgtgc tagggcaaaa aggatttaggc tggatggat ttttggatggat	3540
gttagccctcag tactgggttgc tggatggat gttggatggat gttggatggat gttggatggat	3600
tttgccttgc tttggatggat gttggatggat gttggatggat gttggatggat gttggatggat	3660
tgccatccctt gaaacacggctt ggccacttggg tataactgttgc acaaccgc aacaaaaac	3720
acaaatccctt ggcaactggctt agtctatgtt ctctcaatgtt cttttttgtt tggatggat	3780
cattgttta cattaacgc ccactctgtt ttttgcgtt gaaaggccctt ctctttaatc	3840
aaactcttgcgtt ggcccactgat ttttgcgtt gttttttttt cttttttttt cttttttttt	3900
ccggggcaggc aagggttgcgtt aagatttggc aacgtggctt aattttttttt cttttttttt	3960
agttcaattt catgtttttt gaccctttt tataaaatgtt caatatttctt tttttttttt	4020
cttttcatatg gaatgttattt tcaaatgtt aactctttttt cttttttttt cttttttttt	4080
tgtttttttt cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	4140
ttttaaccttgc tggatggatggc aaacgattttt actagactttt atgtttttttt tttttttttt	4200
aaggggaaattt cttttttttt ccctccaaatgtt tttttttttt tttttttttt tttttttttt	4260
aagttagtgcgtt atctttttttt cttttttttt tttttttttt tttttttttt tttttttttt	4320
ggcattttttt tagaaatgtt aatgttgcgtt tttttttttt tttttttttt tttttttttt	4380
gagacccaaa ggaagaaactg gataaaatctt tccaaatccca aaagcatgag atttttttttt	4440
ccaaatatgc aaaaatgacc caagagaactt ttcttattttt gttttttttt tttttttttt	4500
aagtggaaagg aagaacagttt aatgttgcgtt tttttttttt tttttttttt tttttttttt	4560
aagtatttttta agataagagg gggaaaaaca cataaagtca aacaaaatgtt tttttttttt	4620
ataacagcaa cttttttttt atagactttt atgttgcgtt tttttttttt tttttttttt	4680
acaaagaata agcttgcctt agggctggca acatcttgcgtt tttttttttt tttttttttt	4740
aaatatctt ccaggcaggcc tttttttttt tttttttttt tttttttttt tttttttttt	4800
ttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	4860
cgatcttgcgtt aagacattt tttttttttt tttttttttt tttttttttt tttttttttt	4920
catcttgcgtt aatgttgcgtt tttttttttt tttttttttt tttttttttt tttttttttt	4980
aaagaagaatgtt aatgttgcgtt tttttttttt tttttttttt tttttttttt tttttttttt	5040
ggaaaggactt aagaaaacactt tttttttttt tttttttttt tttttttttt tttttttttt	5100
cagccaaaggaa aaaaatgatactt tttttttttt tttttttttt tttttttttt tttttttttt	5160
atttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5220
atttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5280
atttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5340
tttatggaaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5400
ttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5460
ttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	5520

ttcttatgaca atatgacact tgtaaattgt tgtttcaaaa tgaacagcga agcctaact	5580
ttaaatgaca tttgtattct cagacactga gtagcataaa aaccacatga actgaactgt	5640
aacttaaatt ctt	5653

<210> 2
<211> 923
<212> PRT
<213> human

<400> 2
Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
1 5 10 15
Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
20 25 30
Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
35 40 45
His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
50 55 60
Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
65 70 75 80
Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
85 90 95
Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Val
100 105 110
Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
115 120 125
Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
130 135 140
Pro Glu Cys Ser Gln Asn Tyr Thr Pro Ser Gly Val Ile Lys Ser
145 150 155 160
Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
165 170 175
Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
180 185 190
Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
195 200 205
Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile
210 215 220
Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
225 230 235 240
Gly Ile Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
245 250 255
Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Val Ser Glu Asp
260 265 270
Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
275 280 285
Asp Gln Ile Thr Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu
290 295 300
Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
305 310 315 320
Ser Tyr Arg Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
325 330 335
Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
340 345 350
Tyr Tyr Val Lys Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp
355 360 365
Trp Ile Thr Ile Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn
370 375 380
Thr Asn Pro Thr Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile
385 390 395 400
Thr Arg Phe Val Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser

405	410	415
Met Arg Phe Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser		
420	425	430
Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr		
435	440	445
Ser Ser Asn Gln Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu		
450	455	460
Val Thr Ser Arg Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr		
465	470	475
Ile Asn Glu Trp Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg		
485	490	495
Gly Ile Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met		
500	505	510
Arg Lys Phe Lys Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met		
515	520	525
Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn		
530	535	540
Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg		
545	550	555
Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu		
565	570	575
Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro		
580	585	590
Thr Thr Pro Asn Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala		
595	600	605
Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr		
610	615	620
Thr Val Leu Ala Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln		
625	630	635
Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser		
645	650	655
His Lys Thr Phe Cys His Trp Glu His Asp Asn His Val Gln Leu Lys		
660	665	670
Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly		
675	680	685
Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys		
690	695	700
Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His		
705	710	715
Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu		
725	730	735
Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val		
740	745	750
Trp Met Ala Ile Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val		
755	760	765
Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu		
770	775	780
Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile		
785	790	795
Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp		
805	810	815
Lys Lys Asn Pro Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly		
820	825	830
Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly		
835	840	845
Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met		
850	855	860
Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr		
865	870	875
Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu		
885	890	895
Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp		
900	905	910

Lys Leu Asn Thr Gln Ser Thr Tyr Ser Glu Ala
915 920

<210> 3
<211> 3404
<212> DNA
<213> human

<400> 3

cgatccggca	cgagggaaaa	ataaaagaga	aaaaaacaca	aaagtttaaa	caagaaacct	60
acgaaaccag	ctctggaaag	agccacccctc	tccaaaatgg	atatgttcc	tctcacctgg	120
gttttcttag	cccttactt	tc当地gacac	caagtggag	gccaaccaga	cccaccgtc	180
ggaggtcggt	tgaattccaa	agatgctggc	tatataccct	ctccccggta	cccccaaggac	240
taccctcccc	accagaactg	cgagtggtt	gttacgccc	ccgaacccaa	ccagaagatt	300
gtcctcaact	tcaaccctca	cttggaaatc	gagaagcagc	actgcaagta	tgactttatc	360
gagattcggg	atggggacag	tgaatccgca	gaccccttgg	gcaaacactg	tgggaacatc	420
gccccgcaca	ccatcatctc	ctcgggctcc	atgcttaca	tcaagttcac	ctccgactac	480
gccccggcagg	ggcaggcctt	ctctctgcmc	tacgagatct	tcaagacagg	ctctgaagat	540
tgctcaaaaa	acttccacaag	ccccaaacggg	accatcgaat	cttctgggtt	tcctgagaag	600
tatccacaca	acttggactg	caccccttacc	atsctggcca	aacccaagat	ggagatcatc	660
ctgcagttcc	tgatcttga	cctggagcat	gacccttgc	aggtgggaga	gggggactgc	720
aagtacgati	ggctggacat	ctgggatggc	attccacatg	ttggccccct	gattggcaag	780
tactgtggg	ccaaaacacc	ctctgaactt	cgttcatcga	cggggatcct	ctccctgacc	840
ttcacacgg	acatggcggt	ggccaaggat	ggcttctctg	cgcgttacta	cctggtccac	900
caagagccac	tagagaactt	tcaagtcaat	gttcccttgc	gcatggagtc	tggccggatt	960
gctaataat	agatcagtgc	ctcatctacc	tactctgatg	ggaggtggac	ccctcaacaa	1020
agccggctcc	atgggtatga	caatggctgg	acccccaact	tggattccaa	caaggagttat	1080
ctccaggtgg	acctgcgcctt	ttaaccatg	ctcacggcca	tcgcaacaca	gggagcgtt	1140
tccaggaaaa	cacagaatgg	ctactacgtc	aaatccata	agctggaaat	cagcactaat	1200
ggagggact	ggatgggtgt	ccggcatggc	aaaaaccaca	agtttttca	agccaaacaac	1260
gatgcaactg	agggtgttct	gaacaagctc	cacgctccac	tgtgtacaag	gtttgtttaga	1320
atccggccct	agacttggca	ctcaggatatic	gcccstccggc	tggagctctt	cggctgccgg	1380
gtcagatgt	ctccctgtct	caacatgtct	ggatgtctct	caggcctcat	tgcagactcc	1440
cagatctccg	ctcttccac	ccaggaataac	cttggagcc	ccagtgcagc	ccgcctggc	1500
agcagccgc	cgggctgggt	ccctcgaatc	cctcaggccc	agcccggtga	ggagtggctt	1560
caggtagat	tgggaaacacc	caagacagt	aaaggtgtca	tcatccaggg	agcccgccga	1620
ggagacagta	tcaactgtgt	ggaagccaga	gcattttgtc	gcaagttcaa	agtcttccat	1680
agcctaaac	gcaaggactg	ggaataatatt	caggacccca	ggacccagca	gccaagactg	1740
ttcgaaggga	acatgcacta	tgacacccct	gacatccgaa	gttttgaccc	cattccggca	1800
cagtatgtgc	gggttataccc	ggagagggtgg	tcgcccggc	ggattttggat	ggggctggag	1860
gtgctggct	gtgactggac	agacttccaa	cccacggtag	agacgctggg	acccactgtg	1920
aagagcgaag	agacaaccac	cccttacccc	accgaagagg	ggccacacaa	gtgtggggag	1980
aactgcagct	ttgaggatga	caaagattt	cagctccctt	cgggattcaa	ttgcaacttc	2040
gatttcctg	aggagccctg	tgggtggat	tatgaccatg	ccaaagtggct	ccggaccacc	2100
tgggcccac	gctccagccc	aaacgaccgg	acgtttccag	atgacagggaa	tttcttgcgg	2160
ctgcagatgt	acagccagag	agagggccag	tatgcccggc	tcatcagccc	ccctgtccac	2220
ctgccccgaa	gccccgggt	catggagttc	cagtaccagg	ccacggggcg	ccgggggtg	2280
gcgcgtcgagg	tgggtcgggg	agccagccag	gagagcaat	tgtgtgggt	catccgttag	2340
gaccaggccg	gcgagtgaa	gcacggggcg	atcatctgc	ccagctacga	catggagtag	2400
cagattgtgt	tgcagggagt	gatagggaaa	ggacgttccg	gagagattgc	cattgtatgc	2460
attcggataa	gcactgtatgt	cccactggag	aactgcata	aacccatctc	ggcttttca	2520
ggtgagaatt	ttaaagtgg	catcccgaa	atacatgaga	gagaaggata	tgaagatgaa	2580
attgtatgt	aatacgaggt	ggactggagc	aattcttctt	ctgcaacctc	agggtctggc	2640
gccccctcga	ccgacaaaaga	aaagagctgg	ctgtacaccc	tgatccat	cctcatcacc	2700
atcatcgcca	tgagctca	ggcgctccct	ctgggggcca	cctgtgcagg	cctctgtctc	2760
tactgcac	gttcttactc	ggccctgagc	tcccaagct	gcaccacact	ggagaactac	2820
aacttcgagc	tctacgtgg	ccttaagcac	aaggtaaga	tgaaccacca	aaagtgtgc	2880
tccgaggcat	gacgattgc	acctgaatcc	tatctgacgt	ttcattccag	caagagggc	2940
tgggaaagat	tacattttt	ttcctttgg	aaactgaatg	ccataatctc	gatcaaaccg	3000
atccagaata	ccgaaggat	ggacaggaca	aaaaagcag	tcgcaggagg	aagggagatg	3060
cagccgcaca	ggggatgatt	acccttctag	gaccgcgggt	gctaagtcat	tgcaggaacg	3120
ggggctgtgtt	ctctgtggg	acaaaacagg	agctcatctc	tttggggtca	cagttctatt	3180

ttgtttgtga gtttgtatta ttattattat tattattatt atattttatt tctttggctc
gtgagcaact caaaggaggca gaagaggaga atgactttc cagaatagaa gtggacagt 3240
gatcattatt ctccgcttc tcttctaat caacacttga aaagcaaagt gtctttcag 3300
ccttccatc ttacaaaata aaactcaaaa aagctgtcca gctt 3360
3404

<210> 4
<211> 931
<212> PRT
<213> human

<400> 4
Met Asp Met Phe Pro Leu Thr Trp Val Phe Leu Ala Leu Tyr Phe Ser
1 5 10 15
Arg His Gln Val Arg Gly Gln Pro Asp Pro Pro Cys Gly Arg Leu
20 25 30
Asn Ser Lys Asp Ala Gly Tyr Ile Thr Ser Pro Gly Tyr Pro Gln Asp
35 40 45
Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro
50 55 60
Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys
65 70 75 80
His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu
85 90 95
Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr
100 105 110
Ile Ile Ser Ser Gly Ser Met Leu Tyr Ile Lys Phe Thr Ser Asp Tyr
115 120 125
Ala Arg Gln Gly Ala Gly Phe Ser Leu Arg Tyr Glu Ile Phe Lys Thr
130 135 140
Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile
145 150 155 160
Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr
165 170 175
Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu
180 185 190
Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys
195 200 205
Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro
210 215 220
Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser
225 230 235 240
Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala
245 250 255
Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu
260 265 270
Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile
275 280 285
Ala Asn Glu Gln Ile Ser Ala Ser Ser Thr Tyr Ser Asp Gly Arg Trp
290 295 300
Thr Pro Gln Gln Ser Arg Leu His Gly Asp Asp Asn Gly Trp Thr Pro
305 310 315 320
Asn Leu Asp Ser Asn Lys Glu Tyr Leu Gln Val Asp Leu Arg Phe Leu
325 330 335
Thr Met Leu Thr Ala Ile Ala Thr Gln Gly Ala Ile Ser Arg Glu Thr
340 345 350
Gln Asn Gly Tyr Tyr Val Lys Ser Tyr Lys Leu Glu Val Ser Thr Asn
355 360 365
Gly Glu Asp Trp Met Val Tyr Arg His Gly Lys Asn His Lys Val Phe
370 375 380
Gln Ala Asn Asn Asp Ala Thr Glu Val Val Leu Asn Lys Leu His Ala
385 390 395 400
Pro Leu Leu Thr Arg Phe Val Arg Ile Arg Pro Gln Thr Trp His Ser
405 410 415

Gly Ile Ala Leu Arg Leu Glu Leu Phe Gly Cys Arg Val Thr Asp Ala
420 425 430
Pro Cys Ser Asn Met Leu Gly Met Leu Ser Gly Leu Ile Ala Asp Ser
435 440 445
Gln Ile Ser Ala Ser Ser Thr Gln Glu Tyr Leu Trp Ser Pro Ser Ala
450 455 460
Ala Arg Leu Val Ser Ser Arg Ser Gly Trp Phe Pro Arg Ile Pro Gln
465 470 475 480
Ala Gln Pro Gly Glu Glu Trp Leu Gln Val Asp Leu Gly Thr Pro Lys
485 490 495
Thr Val Lys Gly Val Ile Ile Gln Gly Ala Arg Gly Gly Asp Ser Ile
500 505 510
Thr Ala Val Glu Ala Arg Ala Phe Val Arg Lys Phe Lys Val Ser Tyr
515 520 525
Ser Leu Asn Gly Lys Asp Trp Glu Tyr Ile Gln Asp Pro Arg Thr Gln
530 535 540
Gln Pro Lys Leu Phe Glu Gly Asn Met His Tyr Asp Thr Pro Asp Ile
545 550 555 560
Arg Arg Phe Asp Pro Ile Pro Ala Gln Tyr Val Arg Val Tyr Pro Glu
565 570 575
Arg Trp Ser Pro Ala Gly Ile Gly Met Arg Leu Glu Val Leu Gly Cys
580 585 590
Asp Trp Thr Asp Ser Lys Pro Thr Val Glu Thr Leu Gly Pro Thr Val
595 600 605
Lys Ser Glu Glu Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala Thr
610 615 620
Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu
625 630 635 640
Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly
645 650 655
Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser
660 665 670
Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg
675 680 685
Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser
690 695 700
Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr
705 710 715 720
Gln Ala Thr Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala
725 730 735
Ser Gln Glu Ser Lys Leu Leu Trp Val Ile Arg Glu Asp Gln Gly Gly
740 745 750
Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr Asp Met Glu Tyr
755 760 765
Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg Ser Gly Glu Ile
770 775 780
Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro Leu Glu Asn Cys
785 790 795 800
Met Glu Pro Ile Ser Ala Phe Ala Gly Glu Asn Phe Lys Val Asp Ile
805 810 815
Pro Glu Ile His Glu Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu
820 825 830
Tyr Glu Val Asp Trp Ser Asn Ser Ser Ala Thr Ser Gly Ser Gly
835 840 845
Ala Pro Ser Thr Asp Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro
850 855 860
Ile Leu Ile Thr Ile Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly
865 870 875 880
Ala Thr Cys Ala Gly Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly
885 890 895
Leu Ser Ser Arg Ser Cys Thr Thr Leu Glu Asn Tyr Asn Phe Glu Leu
900 905 910
Tyr Asp Gly Leu Lys His Lys Val Lys Met Asn His Gln Lys Cys Cys

915
Ser Glu Ala
930

920

925

<210> 5
<211> 18
<212> PRT
<213> human

<400> 5
 Phe Arg Asn Asp Glu Cys Gly Asp Thr Ile Lys Ile Glu Asn Pro Gly
 1 5 10 15
 Tyr Leu

<210> 6
<211> 18
<212> PRT
<213> human

<400> 6
 Phe Arg Ser Asp Lys Cys Gly Gly Thr Ile Lys Ile Glu Ser Pro Gly
 1 5 10 15
 Tyr Leu

<210> 7
<211> 24
<212> DNA
<213> human

<400> 7
tttcgcaacg ataaatgtgg cgat

24

<210> 8
<211> 20
<212> DNA
<213> human

<400> 8
tatcactcca ctaggtgttg

20

<210> 9
<211> 20
<212> DNA
<213> human

<400> 9
ccaaaccaqaa qattqtcctc

20

<210> 10
<211> 20
<212> DNA
<213> human

<400> 10
qtaqqtaqat qaggcactqa

20

<210> 11
<211> 44
<212> PRT
<213> human

<400> 11
Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp
1 5 10 15
Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys
20 25 30
Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
35 40

09580802 - 053000